## SEQUENCE LISTING

	(1) GENER	AL INFORMATION:
5	(i) .	APPLICANTS: Chatterjee, Deb K. Solus, Joseph Yang, Shuwei
	(ii) '	TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
	(iii)	NUMBER OF SEQUENCES: 93
10	(iv)	CORRESPONDENCE ADDRESS:  (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  (B) STREET: 1100 New York Ave., N.W., Suite 600  (C) CITY: Washington
15		(D) STATE: DC (E) COUNTRY: USA (F) ZIP: 20005-3934
	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk
20		(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
	(vi)	CURRENT APPLICATION DATA:
		(A) APPLICATION NUMBER: (To be assigned) (B) FILING DATE: 06-FEB-1998
25		(C) CLASSIFICATION:
	(vii)	PRIOR APPLICATION DATA:  (A) APPLICATION NUMBER: (To be assigned)  (B) FILING DATE: 06-JAN-1998  (C) CLASSIFICATION:
30	(vii) P	RIOR APPLICATION DATA:  (A) APPLICATION NUMBER: US 60/037,393  (B) FILING DATE: 07-FEB-1997  (C) CLASSIFICATION:
35	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Esmond, Robert W. (B) REGISTRATION NUMBER: 32,893 (C) REFERENCE/DOCKET NUMBER: 0942.4250002
	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 202-371-2600
40		(B) TELEFAY: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGAGAC TATTTCTCT	TGATGGCACA	GCCCTGGCCT	ACAGGGCATA	TTACGCCCTC	60
GACAGATCCC TTTCCACAT	CACAGGAATT	CCAACGAACG	CCGTCTATGG	CGTTGCCAGG	120
ATGCTCGTTA AATTCATTA	GGAACACATT	ATACCCGAAA	AGGACTACGC	GGCTGTGGCC	180
TTCGACAAGA AGGCAGCGA	C GTTCAGACAC	AAACTGCTCG	TAAGCGACAA	GGCGCAAAGG	240
CCAAAGACTC CGGCTCTTC	r agttcagcag	CTACCTTACA	TCAAGCGGCT	GATAGAAGCT	300
CTTGGTTTCA AAGTGCTGG	A GCTGGAGGGA	TACGAAGCAG	ACGATATCAT	CGCCACGCTT	360
GCAGTCAGGG CTGCACGTT	r tttgatgaga	TTTTCATTAA	TAACCGGTGA	CAAGGATATG	420
CTTCAACTTG TAAACGAGA	A GATAAAGGTC	TGGAGAATCG	TCAAGGGGAT	ATCGGATCTT	480
GAGCTTTACG ATTCGAAAA	A GGTGAAAGAA	AGATACGGTG	TGGAACCACA	TCAGATACCG	540
GATCTTCTAG CACTGACGG	G AGACGACATA	GACAACATTC	CCGGTGTAAC	GGGAATAGGT	600
GAAAAGACCG CTGTACAGC	r TCTCGGCAAG	TATAGAAATC	TTGAATACAT	TCTGGAGCAT	660
GCCCGTGAAC TCCCCCAGA	G AGTGAGAAAG	GCTCTCTTGA	GAGACAGGGA	AGTTGCCATC	720
CTCAGTAAAA AACTTGCAA	C TCTGGTGACG	AACGCACCTG	TTGAAGTGGA	CTGGGAAGAG	780
ATGAAATACA GAGGATACG	A CAAGAGAAAA	CTACTTCCGA	TATTGAAAGA	ACTGGAGTTT	840
GCTTCCATCA TGAAGGAAC	r TCAACTGTAC	GAAGAAGCAG	AACCCACCGG	ATACGAAATC	900
GTGAAGGATC ATAAGACCT	r cgaagatctc	ATCGAAAAGC	TGAAGGAGGT	TCCATCTTTT	960
GCCCTGGACC TTGAAACGT	C CTCCCTTGAC	CCGTTCAACT	GTGAGATAGT	CGGCATCTCC	1020
GTGTCGTTCA AACCGAAAA	C AGCTTATTAC	ATTCCACTTC	ATCACAGAAA	CGCCCAGAAT	1080
CTTGATGAAA CACTGGTGC	T GTCGAAGTTG	AAAGAGATCC	TCGAAGACCC	GTCTTCGAAG	1140
ATTGTGGGTC AGAACCTGA	A GTACGACTAC	AAGGTTCTTA	TGGTAAAGGG	TATATCGCCA	1200
GTTTATCCGC ATTTTGACA	C GATGATAGCT	GCATATTTGC	TGGAGCCAAA	CGAGAAAAA	1260
TTCAATCTCG AAGATCTGT	C TTTGAAATTT	CTCGGATACA	AAATGACGTC	TTATCAGGAA	1320

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CTGATGTCGT	TTTCCTCACC	ACTTTTTGGT	TTCAGCTTTG	CGGATGTTCC	GGTAGACAAG	1380
GCTGCGAACT	ACTCCTGCGA	GGATGCAGAC	ATCACTTATA	GGCTCTACAA	GATACTCAGC	1440
ATGAAGCTCC	ATGAAGCGGA	ACTTGAGAAC	GTCTTCTACA	GGATAGAGAT	GCCGTTGGTG	1500
AACGTTCTTG	CACGCATGGA	ATTGAACGGG	GTGTATGTGG	ACACAGAATT	CCTGAAAAAG	1560
CTCTCGGAGG	AGTACGGCAA	AAAGCTCGAG	GAACTGGCCG	AAAAAATCTA	CCAGATAGCA	1620
GGTGAGCCCT	TCAACATCAA	TTCTCCAAAA	CAGGTTTCAA	AGATCCTTTT	TGAGAAGCTG	1680
GGAATAAAAC	CCCGTGGAAA	AACGACAAAA	ACAGGAGAGT	ACTCTACCAG	GATAGAGGTG	1740
TTGGAAGAGA	TAGCGAATGA	GCACGAGATA	GTACCCCTCA	TTCTCGAGTA	CAGAAAGATC	1800
CAGAAACTGA	AATCGACCTA	CATAGACACC	CTTCCGAAAC	TTGTGAACCC	GAAAACCGGA	1860
AGAATTCATG	CATCTTTCCA	CCAGACGGGT	ACCGCCACTG	GCAGGTTGAG	TAGCAGTGAT	1920
CCAAATCTTC	AGAATCTTCC	GACAAAGAGC	GAAGAGGGAA	AAGAAATTAG	AAAAGCGATT	1980
GTGCCCCAGG	ATCCAGACTG	GTGGATCGTC	AGTGCGGATT	ATTCCCAAAT	AGAACTCAGA	2040
ATCCTCGCTC	ATCTCAGTGG	TGATGAGAAC	CTTGTGAAGG	CCTTCGAGGA	GGGCATCGAT	2100
GTGCACACCT	TGACTGCCTC	CAGGATCTAC	AACGTAAAGC	CAGAAGAAGT	GAACGAAGAA	2160
ATGCGACGGG	TTGGAAAGAT	GGTGAACTTC	TCTATAATAT	ACGGTGTCAC	ACCGTACGGT	2220
CTTTCTGTGA	GACTTGGAAT	ACCGGTTAAA	GAAGCAGAAA	AGATGATTAT	CAGCTATTTC	2280
ACACTGTATC	CAAAGGTGCG	AAGCTACATC	CAGCAGGTTG	TTGCAGAGGC	AAAAGAGAAG	2340
GGCTACGTCA	GGACTCTCTT	TGGAAGAAAA	AGAGATATTC	CCCAGCTCAT	GGCAAGGGAC	2400
AAGAACACCC	AGTCCGAAGG	CGAAAGAATC	GCAATAAACA	CCCCCATTCA	GGGAACGGCG	2460
GCAGATATAA	TAAAATTGGC	TATGATAGAT	ATAGACGAGG	AGCTGAGAAA	AAGAAACATG	2520
AAATCCAGAA	TGATCATTCA	GGTTCATGAC	GAACTGGTCT	TCGAGGTTCC	CGATGAGGAA	2580
AAAGAAGAAC	TAGTTGATCT	GGTGAAGAAC	AAAATGACAA	ATGTGGTGAA	ACTCTCTGTG	2640
CCTCTTGAGG	TTGACATAAG	CATCGGAAAA	AGCTGGTCTT	GA		2682

## (2) INFORMATION FOR SEQ ID NO:2:

- 25 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 893 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: protein

		(xi)	SEQU	JENCE	E DES	CRIF	OIT	: SE	EQ II	NO:	2:						
		Met 1	Ala	Arg	Leu	Phe 5	Leu	Phe	Asp	Gly	Thr 10	Ala	Leu	Ala	Tyr	Arg 15	Ala
	5	Tyr	Tyr	Ala	Leu 20	Asp	Arg	Ser	Leu	Ser 25	Thr	Ser	Thr	Gly	Ile 30	Pro	Thr
		Asn	Ala	Val 35	Tyr	Gly	Val	Ala	Arg 40	Met	Leu	Val	Lys	Phe 45	Ile	Lys	Glu
	10	His	Ile 50	Ile	Pro	Glu	Lys	Asp 55	Tyr	Ala	Ala	Val	Ala 60	Phe	Asp	Lys	Lys
J		Ala 65	Ala	Thr	Phe	Arg	His 70	Lys	Leu	Leu	Val	Ser 75	Asp	Lys	Ala	Gln	Arg 80
		Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg
Man Ami						85					90					95	
	15	Leu	Ile	Glu	Ala 100	Leu	Gly	Phe	Lys	Val 105	Leu	Glu	Leu	Glu	Gly 110	Tyr	Glu
		Ala	Asp	Asp 115	Ile	Ile	Ala	Thr	Leu 120	Ala	Val	Arg	Ala	Ala 125	Arg	Phe	Leu
Figure 1	20	Met	Arg 130	Phe	Ser	Leu	Ile	Thr 135	Gly	Asp	Lys	Asp	Met 140	Leu	Gln	Leu	Val
		Asn 145	Glu	Lys	Ile	Lys	Val 150	Trp	Arg	Ile	Val	Lys 155	Gly	Ile	Ser	Asp	Leu 160
		Glu	Leu	Tyr	Asp	Ser 165	Lys	Lys	Val	Lys	Glu 170	Arg	Tyr	Gly	Val	Glu 175	Pro
	25	His	Gln	Ile	Pro 180	Asp	Leu	Leu	Ala	Leu 185	Thr	Gly	Asp	Asp	Ile 190	Asp	Asn
		Ile	Pro	Gly 195	Val	Thr	Gly	Ile	Gly 200		Lys	Thr	Ala	Val 205	Gln	Leu	Leu
	30	Gly	Lys 210	_	Arg	Asn	Leu	Glu 215		Ile	Leu	Glu	His 220	Ala	Arg	Glu	Leu
		Pro 225		Arg	Val	Arg	Lys 230		Leu	Leu	Arg	Asp 235	Arg	Glu	Val	Ala	Ile 240
		Lev	Ser	Lys	Lys	Leu 245		Thr	Leu	Val	Thr 250		Ala	Pro	Val	Glu 255	Val

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu

560 555 550 545 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro 5 580 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile 600 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp 10 630 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile 650 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala 15 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp 680 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu 695 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu 20 715 710 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala 25 745 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp 30 790 785 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile 810 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp 35 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val 835 840

			His	Asp 850	Glu	Leu	Val	Phe	Glu 855	Val	Pro	Asp	Glu	Glu 860	Lys	Glu	Glu	Leu
			Val 865	Asp	Leu	Val	Lys	Asn 870	Lys	Met	Thr	Asn	Val 875	Val	Lys	Leu	Ser	Val 880
	5		Pro	Leu	Glu	Val	Asp 885	Ile	Ser	Ile	Gly	Lys 890	Ser	Trp	Ser			
		(2)	INFO	TAMS	ON F	FOR S	SEQ I	D NO	):3:									
	10		(i)	(B)	LEN TYP STF	NGTH: PE: 8 RANDI	: 677	7 ami o aci SS: r	ino a id not 1	acids celev								
			(ii)	MOLE	ECULE	E TYI	PE: p	prote	ein									
			(xi)	SEQU	JENCE	E DES	SCRII	PTIO	1: SI	EQ II	ONO:	:3:						
	15		Met 1	Ser	Leu	His	Ala 5	Arg	Glu	Leu	Pro	Gln 10	Arg	Val	Arg	Lys	Ala 15	Leu
The first from the first fair			Leu	Arg	Asp	Arg 20	Glu	Val	Ala	Ile	Leu 25	Ser	Lys	Lys	Leu	Ala 30	Thr	Leu
	20		Val	Thr	Asn 35	Ala	Pro	Val	Glu	Val 40	Asp	Trp	Glu	Glu	Met 45	Lys	Tyr	Arg
			Gly	Tyr 50	Asp	Lys	Arg	Lys	Leu 55	Leu	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe
			Ala 65	Ser	Ile	Met	Lys	Glu 70	Leu	Gln	Leu	Tyr	Glu 75	Glu	Ala	Glu	Pro	Thr 80
	25		Gly	Tyr	Glu	Ile	Val 85	_	_	His	_	Thr 90	Phe	Glu	Asp	Leu	Ile 95	Glu
			Lys	Leu	Lys	Glu 100		Pro	Ser	Phe	Ala 105	Leu	Ala	Leu	Glu	Thr 110	Ser	Ser
	30		Leu	Asp	Pro 115	Phe	Asn	Сув	Glu	Ile 120	Val	Gly	Ile	Ser	Val 125	Ser	Phe	Lys
			Pro	Lys 130	Thr	Ala	Tyr	Tyr	Ile 135	Pro	Leu	His	His	Arg 140	Asn	Ala	Gln	Asn
			Leu 145	Asp	Glu	Thr	Leu	Val 150		Ser	Lys	Leu	Lys 155		Ile	Leu	Glu	Asp 160

		Pro	Ser	Ser	Lys	Ile 165	Val	Gly	Gln	Asn	Leu 170	Lys	Tyr	Asp	Tyr	Lys 175	Val
		Leu	Met	Val	Lys 180	Gly	Ile	Ser	Pro	Val 185	Tyr	Pro	His	Phe	Asp 190	Thr	Met
	5	Ile	Ala	Ala 195	Tyr	Leu	Leu	Glu	Pro 200	Asn	Glu	Lys	Lys	Phe 205	Asn	Leu	Glu
		Asp	Leu 210	Ser	Leu	Lys	Phe	Leu 215	Gly	Tyr	Lys	Met	Thr 220	Ser	Tyr	Gln	Glu
1	10	Leu 225	Met	Ser	Phe	Ser	Ser 230	Pro	Leu	Phe	Gly	Phe 235	Ser	Phe	Ala	Asp	Val 240
		Pro	Val	Asp	Lys	Ala 245	Ala	Asn	Tyr	Ser	Cys 250	Glu	Asp	Ala	Asp	Ile 255	Thr
J		Tyr	Arg	Leu	Tyr 260	Lys	Ile	Leu	Ser	Met 265	Lys	Leu	His	Glu	Ala 270	Glu	Leu
	15	Glu	Asn	Val 275	Phe	Tyr	Arg	Ile	Glu 280	Met	Pro	Leu	Val	Asn 285	Val	Leu	Ala
#J		Arg	Met 290	Glu	Leu	Asn	Gly	Val 295	Tyr	Val	Asp	Thr	Glu 300	Phe	Leu	Lys	Lys
	20	Leu 305	Ser	Glu	Glu	Tyr	Gly 310	Lys	Lys	Leu	Glu	Glu 315	Leu	Ala	Glu	Lys	Ile 320
		Tyr	Gln	Ile	Ala	Gly 325	Glu	Pro	Phe	Asn	11e 330	Asn	Ser	Pro	Lys	Gln 335	Val
		Ser	Lys	Ile	Leu 340	Phe	Glu	Lys	Leu	Gly 345	Ile	Lys	Pro	Arg	Gly 350	Lys	Thr
2	25	Thr	Lys	Thr 355	Gly	Glu	Tyr	Ser	Thr 360	Arg	Ile	Glu	۷al	Leu 365	Glu	Glu	Ile
		Ala	Asn 370	Glu	His	Glu	Ile	Val 375	Pro	Leu	Ile	Leu	Glu 380	Tyr	Arg	Lys	Ile
:	30	Gln 385	Lys	Leu	Lys	Ser	Thr 390	Tyr	Ile	Asp	Thr	Leu 395	Pro	Lys	Leu	Val	Asn 400
		Pro	Lys	Thr	Gly	Arg 405	Ile	His	Ala	Ser	Phe 410	His	Gln	Thr	Gly	Thr 415	Ala
		Thr	Gly	Arg	Leu 420	Ser	Ser	Ser	Asp	Pro 425	Asn	Leu	Gln	Asn	Leu 430	Pro	Thr
;	35	Lys	Ser	Glu 435	Glu	Gly	Lys	Glu	Ile 440	Arg	Lys	Ala	Ile	Val 445	Pro	Gln	Asp
		Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg

Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu

455

470

460

475

	5	Glu	Gly	Ile	Asp	Val 485	His	Thr	Leu	Thr	Ala 490	Ser	Arg	Ile	Tyr	Asn 495	Val
		Lys	Pro	Glu	Glu 500	Val	Asn	Glu	Glu	Met 505	Arg	Arg	Val	Gly	Lys 510	Met	Val
٠		Asn	Phe	Ser 515	Ile	Ile	Tyr	Gly	Val 520	Thr	Pro	Tyr	Gly	Leu 525	Ser	Val	Arg
	10	Leu	Gly 530	Ile	Pro	Val	Lys	Glu 535	Ala	Glu	Lys	Met	Ile 540	Ile	Ser	Tyr	Phe
		Thr 545	Leu	Tyr	Pro	Lys	Val 550	Arg	Ser	Tyr	Ile	Gln 555	Gln	Val	Val	Ala	Glu 560
No. In	15	Ala	Lys	Glu	Lys	Gly 565	Tyr	Val	Arg	Thr	Leu 570	Phe	Gly	Arg	Lys	Arg 575	Asp
		Ile	Pro	Gln	Leu 580	Met	Ala	Arg	Asp	Lys 585	Asn	Thr	Gln	Ser	Glu 590	Gly	Glu
		Arg	Ile	Ala 595	Ile	Asn	Thr	Pro	Ile 600	Gln	Gly	Thr	Ala	Ala 605	Asp	Ile	Ile
	20	Lys	Leu 610	Ala	Met	Ile	Asp	Ile 615	Asp	Glu	Glu	Leu	Arg 620	Lys	Arg	Asn	Met
		Lys 625	Ser	Arg	Met	Ile	11e 630	Gln	Val	His	Asp	Glu 635	Leu	Val	Phe	Glu	Val 640
	25	Pro	Asp	Glu	Glu	Lys 645	Glu	Glu	Leu	Val	Asp 650	Leu	Val	Lys	Asn	Lys 655	Met
		Thr	Asn	Val	Val 660	Lys	Leu	Ser	Val	Pro 665	Leu	Glu	Val	Asp	Ile 670	Ser	Ile
		Gly	Lys	Ser	Trp	Ser											

(ii) MOLECULE TYPE: protein

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(A) LENGTH: 610 amino acids

(D) TOPOLOGY: not relevant

(C) STRANDEDNESS: not relevant

675

(2) INFORMATION FOR SEQ ID NO:4:

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450

	(xi)	SEQ	JENCE	E DES	SCRIE	OIT	1: SE	Q II	NO:	:4:						
	Met 1	Lys	Glu	Leu	Gln 5	Leu	Tyr	Glu	Glu	Ala 10	Glu	Pro	Thr	Gly	Tyr 15	Glu
5	Ile	Val	Lys	Asp 20	His	Lys	Thr	Phe	Glu 25	Asp	Leu	Ile	Glu	Lys 30	Leu	Lys
	Glu	Val	Pro 35	Ser	Phe	Ala	Leu	Ala 40	Leu	Glu	Thr	Ser	Ser 45	Leu	Asp	Pro
	Phe	Asn 50	Cys	Glu	Ile	Val	Gly 55	Ile	Ser	Val	Ser	Phe 60	Lys	Pro	Lys	Thr
10	Ala 65	Tyr	Tyr	Ile	Pro	Leu 70	His	His	Arg	Asn	Ala 75	Gln	Asn	Leu	Asp	Glu 80
	Thr	Leu	Val	Leu	Ser 85	Lys	Leu	Lys	Glu	Ile 90	Leu	Glu	Asp	Pro	Ser 95	Ser
15	Lys	Ile	Val	Gly 100	Gln	Asn	Leu	Lys	Tyr 105	Asp	Tyr	Lys	Val	Leu 110	Met	Val
	Lys	Gly	Ile 115	Ser	Pro	Val	Tyr	Pro 120	His	Phe	Asp	Thr	Met 125	Ile	Ala	Ala
	Tyr	Leu 130	Leu	Glu	Pro	Asn	Glu 135	Lys	Lys	Phe	Asn	Leu 140	Glu	Asp	Leu	Ser
20	Leu 145	_	Phe	Leu	Gly	Tyr 150	Lys	Met	Thr	Ser	Tyr 155	Gln	Glu	Leu	Met	Ser 160
	Phe	Ser	Ser	Pro	Leu 165	Phe	Gly	Phe	Ser	Phe 170	Ala	Asp	Val	Pro	Val 175	Asp
25	Lys	Ala	Ala	Asn 180	Tyr	Ser	Сув	Glu	Asp 185	Ala	Asp	Ile	Thr	Tyr 190	Arg	Leu
	Tyr	Lys	Ile 195	Leu	Ser	Met	Lys	Leu 200	His	Glu	Ala	Glu	Leu 205	Glu	Asn	Val
	Phe	Tyr 210		Ile	Glu	Met	Pro 215	Leu	Val	Asn	Val	Leu 220	Ala	Arg	Met	Glu
30	Leu 225		Gly	Val	Tyr	Val 230	Asp	Thr	Glu	Phe	Leu 235	Lys	Lys	Leu	Ser	Glu 240
	Glu	Tyr	Gly	Lys	Lys 2 <b>4</b> 5		Glu	Glu	Leu	Ala 250	Glu	Lys	Ile	Tyr	Gln 255	Ile
35	Ala	Gly	Glu	Pro 260	Phe	Asn	Ile	Asn	Ser 265		Lys	Gln	Val	Ser 270	Lys	Ile
	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr

			275					280					285			
	Gly	Glu 290	Tyr	Ser	Thr	Arg	Ile 295	Glu	Val	Leu	Glu	Glu 300	Ile	Ala	Asn	Glu
5	His 305	Glu	Ile	Val	Pro	Leu 310	Ile	Leu	Glu	Tyr	Arg 315	Lys	Ile	Gln	Lys	Leu 320
	Lys	Ser	Thr	Tyr	Ile 325	qaA	Thr	Leu	Pro	Lys 330	Leu	Val	Asn	Pro	Lys 335	Thr
	Gly	Arg	Ile	His 340	Ala	Ser	Phe	His	Gln 345	Thr	Gly	Thr	Ala	Thr 350	Gly	Arg
10	Leu	Ser	Ser 355	Ser	Asp	Pro	Asn	Leu 360	Gln	Asn	Leu	Pro	Thr 365	Lys	Ser	Glu
	Glu	Gly 370	Lys	Glu	Ile	Arg	Lys 375	Ala	Ile	Val	Pro	Gln 380	Asp	Pro	Asp	Trp
15	Trp 385	Ile	Val	Ser	Ala	Asp 390	Tyr	Ser	Gln	Ile	Glu 395	Leu	Arg	Ile	Leu	Ala 400
	His	Leu	Ser	Gly	Asp 405	Glu	Asn	Leu	Val	Lys 410	Ala	Phe	Glu	Glu	Gly 415	Ile
	Asp	Val	His	Thr 420	Leu	Thr	Ala	Ser	Arg 425	Ile	Tyr	Asn	Val	Lys 430	Pro	Glu
20	Glu	Val	Asn 435	Glu	Glu	Met	Arg	Arg 440	Val	Gly	Lys	Met	Val 445	Asn	Phe	Ser
	Ile	Ile 450	Tyr	Gly	Val	Thr	Pro 455	Tyr	Gly	Leu	Ser	Val 460	Arg	Leu	Gly	Ile
25	Pro 465	Val	Lys	Glu	Ala	Glu 470	Lys	Met	Ile	Ile	Ser 475	Tyr	Phe	Thr	Leu	Tyr 480
	Pro	Lys	Val	Arg	Ser 485	Tyr	Ile	Gln	Gln	Val 490	Val	Ala	Glu	Ala	Lys 495	Glu
30	Lys	Gly	Tyr	Val 500	Arg	Thr	Leu	Phe	Gly 505	Arg	Lys	Arg	Asp	Ile 510	Pro	Gln
	Leu	Met	Ala 515	Arg	Asp	Lys	Asn	Thr 520	Gln	Ser	Glu	Gly	Glu 525	Arg	Ile	Ala
	Ile	Asn 530	Thr	Pro	Ile	Gln	Gly 535	Thr	Ala	Ala	Asp	Ile 540	Ile	Lys	Leu	Ala
35	Met 545	Ile	Asp	Ile	Asp	Glu 550	Glu	Leu	Arg	Lys	Arg 555	Asn	Met	Lys	Ser	Arg 560
	Met	Ile	Ile	Gln	Va1	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu

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575 570 565 Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 585 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 610 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 708 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile 20 Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val 50 Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala 90 Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys

120

Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu

Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro

	145			150					155					160
	Lys Thr	Ala Ty	r Tyr 165	Ile	Pro	Leu	His	His 170	Arg	Asn	Ala	Gln	Asn 175	Leu
5	Asp Glu	Thr Le		Leu	Ser	Lys	Leu 185	Lys	Glu	Ile	Leu	Glu 190	Asp	Pro
	Ser Ser	Lys Il 195	e Val	Gly	Gln	Asn 200	Leu	Lys	Tyr	Asp	Tyr 205	Lys	Val	Leu
	Met Val	. Lys Gl	y Ile	Ser	Pro 215	Val	Tyr	Pro	His	Phe 220	qaA	Thr	Met	Ile
10	Ala Ala 225	Tyr Le	u Leu	Glu 230	Pro	Asn	Glu	Lys	Lys 235	Phe	Asn	Leu	Glu	Asp 240
	Leu Ser	Leu Ly	s Phe 245		Gly	Tyr	Lys	Met 250	Thr	Ser	Tyr	Gln	Glu 255	Leu
15	Met Sei	Phe Se		Pro	Leu	Phe	Gly 265	Phe	Ser	Phe	Ala	Asp 270	Val	Pro
	Val Asp	Lys Al 275	a Ala	Asn	Tyr	Ser 280	Cys	Glu	Asp	Ala	Asp 285	Ile	Thr	Tyr
	Arg Let 290	ı Tyr Ly	s Ile	Leu	Ser 295	Met	Lys	Leu	His	Glu 300	Ala	Glu	Leu	Glu
20	Asn Val	l Phe Ty	r Arg	Ile 310	Glu	Met	Pro	Leu	Val 315	Asn	Val	Leu	Ala	Arg 320
	Met Gl	ı Leu As	n Gly 325		Tyr	Val	Asp	Thr 330	Glu	Phe	Leu	Lys	Lys 335	Leu
25	Ser Gl	ı Glu Ty 34		Lys	Lys	Leu	Glu 345	Glu	Leu	Ala	Glu	Lys 350	Ile	Tyr
	Gln Ile	e Ala Gl 355	y Glu	Pro	Phe		Ile			Pro	Lys 365	Gln	Val	Ser
	Lys Il	e Leu Pl O	e Glu	Lys	Leu 375		Ile	Lys	Pro	Arg 380		Lys	Thr	Thr
30	Lys Th 385	r Gly G	и Туг	Ser 390		Arg	Ile	Glu	Val 395	Leu	Glu	Glu	Ile	Ala 400
	Asn Gl	u His G	u Ile 405		Pro	Leu	Ile	Leu 410		Tyr	Arg	Lys	Ile 415	
35	Lys Le	u Lys So 4:		Tyr	lle	Asp	Thr 425		Pro	Lys	Leu	Val 430		Pro
	Lys Th	r Gly A	g Ile	e His	Ala	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr

445 440 435 Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro 5 470 465 Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu 505 Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys 10 Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu 15 550 Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr 570 Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala 580 Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile 20 600 Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg 615 Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys 25 630 625 Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys 650 Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro 30 Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 35 705

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(A) LENGTH: 893 amino acids

(C) STRANDEDNESS: not relevant

5		(D)	TOF	OLOG	Y: r	ot r	elev	rant								
	(ii)	MOLE	CULE	TYP	E: p	epti	.de									
	(xi)	SEQU	JENCE	E DES	CRIE	OIT	1: SE	EQ II	ONO:	6:						
	Met 1	Ala	Arg	Leu	Phe 5	Leu	Phe	Asp	Gly	Thr 10	Ala	Leu	Ala	Tyr	Arg 15	Ala
10	Tyr	Tyr	Ala	Leu 20	Asp	Arg	Ser	Leu	Ser 25	Thr	Ser	Thr	Gly	Ile 30	Pro	Thr
	Asn	Ala	Val 35	Tyr	Gly	Val	Ala	Arg 40	Met	Leu	Val	Lys	Phe 45	Ile	Lys	Glu
15	His	Ile 50	Ile	Pro	Glu	Lys	Asp 55	Tyr	Ala	Ala	Val	Ala 60	Phe	Asp	Lys	Lys
	Ala 65	Ala	Thr	Phe	Arg	His 70	Lys	Leu	Leu	Val	Ser 75	Asp	Lys	Ala	Gln	Arg 80
	Pro	Lys	Thr	Pro	Ala 85	Leu	Leu	Val	Gln	Gln 90	Leu	Pro	Tyr	Ile	Lys 95	Arg
20	Leu	Ile	Glu	Ala 100	Leu	Gly	Phe	Lys	Val 105	Leu	Glu	Leu	Glu	Gly 110	Tyr	Glu
	Ala	Asp	Asp 115	Ile	Ile	Ala	Thr	Leu 120	Ala	Val	Arg	Ala	Ala 125	Arg	Phe	Leu
25	Met	Arg 130	Phe	Ser	Leu	Ile	Thr 135	Gly	Ala	Lys	Asp	Met 140	Leu	Gln	Leu	Val
	Asn 145	Glu	Lys	Ile	Lys	Val 150	Trp	Arg	Ile	Val	Lys 155	Gly	Ile	Ser	Asp	Leu 160
	Glu	Leu	Tyr	Asp	Ser 165	Lys	Lys	Val	Lys	Glu 170	Arg	Tyr	Gly	Val	Glu 175	Pro
30	His	Gln	Ile	Pro 180	Asp	Leu	Leu	Ala	Leu 185		Gly	Asp	Asp	Ile 190	Asp	Asn
	Ile	Pro	Gly 195	Val	Thr	Gly	Ile	Gly 200		Lys	Thr	Ala	Val 205	Gln	Leu	Leu
35	Gly	Lys 210	Tyr	Arg	Asn	Leu	Glu 215		Ile	Leu	Glu	His 220	Ala	Arg	Glu	Leu

	Pro 225	Gln	Arg	Val	Arg	Lys 230	Ala	Leu	Leu	Arg	Asp 235	Arg	Glu	Val	Ala	Ile 240
	Leu	Ser	Lys	Lys	Leu 245	Ala	Thr	Leu	Val	Thr 250	Asn	Ala	Pro	Val	Glu 255	Val
5	Asp	Trp	Glu	Glu 260	Met	Lys	Tyr	Arg	Gly 265	Tyr	Asp	Lys	Arg	Lys 270	Leu	Leu
	Pro	Ile	Leu 275	Lys	Glu	Leu	Glu	Phe 280	Ala	Ser	Ile	Met	Lys 285	Glu	Leu	Gln
10	Leu	Tyr 290	Glu	Glu	Ala	Glu	Pro 295	Thr	Gly	Tyr	Glu	Ile 300	Val	Lys	Asp	His
	Lys 305	Thr	Phe	Glu	Asp	Leu 310	Ile	Glu	Lys	Leu	Lys 315	Glu	Val	Pro	Ser	Phe 320
	Ala	Leu	Ala	Leu	Glu 325	Thr	Ser	Ser	Leu	Asp 330	Pro	Phe	Asn	Cys	Glu 335	Ile
15	Val	Gly	Ile	Ser 340	Val	Ser	Phe	Lys	Pro 345	Lys	Thr	Ala	Tyr	Tyr 350	Ile	Pro
	Leu	His	His 355	Arg	Asn	Ala	Gln	Asn 360	Leu	Asp	Glu	Thr	Leu 365	Val	Leu	Ser
20	Lys	Leu 370	Lys	Glu	Ile	Leu	Glu 375	Asp	Pro	Ser	Ser	Lys 380	Ile	Val	Gly	Gln
	Asn 385		Lys	Tyr	Asp	Tyr 390	Lys	Val	Leu	Met	Val 395	Lys	Gly	Ile	Ser	Pro 400
	Val	Туr	Pro	His	Phe 405	Asp	Thr	Met	Ile	Ala 410		Tyr	Leu	Leu	Glu 415	Pro
25	Asn	Glu	Lys	Lys 420		Asn	Leu	Glu	Asp 425	Leu	Ser	Leu	Lys	Phe 430	Leu	Gly
	Tyr	Lys	Met 435		Ser	Tyr	Gln	Glu 440		Met	Ser	Phe	Ser 445		Pro	Leu
30	Phe	Gly 450		Ser	Phe	Ala	Asp 455		Pro	۷al	Asp	Lys 460		Ala	Asn	Tyr
	Ser 465		Glu	Asp	Ala	Asp 470		Thr	Tyr	Arg	Leu 475		Lys	Ile	Leu	Ser 480
	Met	Lys	Leu	His	Glu 485		Glu	Leu	Glu	490		Phe	Tyr	Arg	Ile 495	Glu
35	Met	Pro	Leu	Val 500		. Val	Leu	Ala	Arg		Glu	Leu	Asn	Gly 510		Tyr

													_		_	_
	Val	Asp	Thr 515	Glu	Phe	Leu	Lys	Lys 520	Leu	Ser	Glu	Glu	Tyr 525	Gly	Lys	Lys
	Leu	Glu 530	Glu	Leu	Ala	Glu	Lys 535	Ile	Tyr	Gln	Ile	Ala 540	Gly	Glu	Pro	Phe
5	Asn 545	Ile	Asn	Ser	Pro	Lys 550	Gln	Val	Ser	Lys	Ile 555	Leu	Phe	Glu	Lys	Leu 560
	Gly	Ile	Lys	Pro	Arg 565	Gly	Lys	Thr	Thr	Lys 570	Thr	Gly	Glu	Tyr	Ser 575	Thr
10	Arg	Ile	Glu	Val 580	Leu	Glu	Glu	Ile	Ala 585	Asn	Glu	His	Glu	Ile 590	Val	Pro
	Leu	Ile	Leu 595	Glu	Tyr	Arg	Lys	Ile 600	Gln	Lys	Leu	Lys	Ser 605	Thr	Tyr	Ile
	Asp	Thr 610	Leu	Pro	Lys	Leu	Val 615	Asn	Pro	Lys	Thr	Gly 620	Arg	Ile	His	Ala
15	Ser 625	Phe	His	Gln	Thr	Gly 630	Thr	Ala	Thr	Gly	Arg 635	Leu	Ser	Ser	Ser	Asp 640
	Pro	Asn	Leu	Gln	Asn 645	Leu	Pro	Thr	Lys	Ser 650	Glu	Glu	Gly	Lys	Glu 655	Ile
20	Arg	Lys	Ala	Ile 660	Val	Pro	Gln	Asp	Pro 665	Asp	Trp	Trp	Ile	Val 670	Ser	Ala
	Asp	Tyr	Ser 675	Gln	Ile	Glu	Leu	Arg 680		Leu	Ala	His	Leu 685	Ser	Gly	Asp
	Glu	Asn 690		Val	Lys	Ala	Phe 695	Glu	Glu	Gly	Ile	Asp 700		His	Thr	Leu
25	Thr 705		Ser	Arg	Ile	Tyr 710		Val	Lys	Pro	Glu 715		Val	Asn	Glu	Glu 720
	Met	Arg	Arg	Val	Gly 725		Met	Val	Asn	Phe 730		Ile	Ile	Tyr	Gly 735	Val
30	Thr	Pro	Tyr	Gly 740		Ser	Val	Arg	Leu 745		Ile	Pro	Val	Lys 750		Ala
	Glu	Lys	Met 755		Ile	Ser	Туг	Phe 760		Leu	Tyr	Pro	765		Arg	Ser
	Tyr	770		Gln	Val	. Val	Ala 775		Ala	Lys	Glu	Lys 780		туг	Val	Arg
35	Thr 785		ı Phe	e Gly	Arg	790		Asp	ıle	Pro	795		ı Met	Ala	Arg	Asp 800

		Lys	Asn	Thr	Gln	805	Glu	GIY	GIU	Arg	810	Ala	116	Apri	1111	815	
		Gln	Gly	Thr	Ala 820	Ala	Asp	Ile	Ile	Lys 825	Leu	Ala	Met	Ile	Asp 830	Ile	Asp
5		Glu	Glu	Leu 835	Arg	Lys	Arg	Asn	Met 840	Lys	Ser	Arg	Met	Ile 845	Ile	Gln	Val
		His	Asp 850	Glu	Leu	Val	Phe	Glu 855	Val	Pro	Asp	Glu	Glu 860	Lys	Glu	Glu	Leu
10		Val 865	Asp	Leu	Val	Lys	Asn 870	Lys	Met	Thr	Asn	Val 875	Val	Lys	Leu	Ser	Val 880
		Pro	Leu	Glu	Val	Asp 885	Ile	Ser	Ile	Gly	Lys 890	Ser	Trp	Ser			
	(2)	INFO	RMAT:	ION :	FOR S	SEQ :	ID N	0:7:									
15		(i)	(A (B (C	) LE: ) TY ) ST	E CHA NGTH PE: ( RAND) POLO(	: 89: amin EDNE	3 am o ac SS:	ino a id not :	acid rele								
20					E TY				EO T	D NO	• 7 •						
20												Ala	Leu	ı Ala	Tyr	Arg 15	Ala
		Tyr	Tyr	Ala	Leu 20	Asp	Arg	Ser	Leu	Ser 25	Thr	Ser	Thr	Gly	Ile 30	Pro	Thr
25		Asn	Ala	Val	L Tyr	Gly	v Val	Ala	Arg	Met	Leu	ı Val	. Lys	Phe 45	e Ile	Lys	Glu
		His	50	e Ile	e Pro	Glu	ı Lys	Asp 55	Туг	Ala	Ala	ı Val	. Ala	a Phe	e Asp	Lys	Lys
30		Ala 65	a Ala	a Thi	r Phe	e Arg	7 His	s Lys	: Let	ı Lev	. Val	1 Ser 75	as,	p Ly:	s Ala	Glr	Arg 80
		Pro	) Ly	s Th	r Pro	85	a Le	ı Lev	ı Val	L Glr	90	ı Lev	ı Pro	о Ту:	r Ile	95	arg
		Le	ı Ile	e Gl	u Ala 100		u Gl	y Phe	e Ly:	3 Val		u Glu	ı Le	u Gl	u Gly 110	, <b>Ty</b> 1	c Glu
35		Ala	a Asj	p As	p Ile	e Il	e Ala	a Thi	c Le	Ala	a Va	l Ar	g Al	a Al	a Arg	g Phe	e Leu

115

125

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro

410

405

	Asn	Glu	Lys	Lys 420	Phe	Asn	Leu	Glu	Asp 425	Leu	Ser	Leu	Lys	Phe 430	Leu	Gly
	Tyr	Lys	Met 435	Thr	Ser	Tyr	Gln	Glu 440	Leu	Met	Ser	Phe	Ser 445	Ser	Pro	Leu
5	Phe	Gly 450	Phe	Ser	Phe	Ala	Asp 455	Val	Pro	Val	Asp	Lys 460	Ala	Ala	Asn	Tyr
	Ser 465	Cys	Glu	Asp	Ala	Asp 470	Ile	Thr	Tyr	Arg	Leu 475	Tyr	Lys	Ile	Leu	Ser 480
10	Met	Lys	Leu	His	Glu 485	Ala	Glu	Leu	Glu	Asn 490	Val	Phe	Tyr	Arg	Ile 495	Glu
	Met	Pro	Leu	Val 500	Asn	Val	Leu	Ala	Arg 505	Met	Glu	Leu	Asn	Gly 510	Val	Tyr
	Val	Asp	Thr 515	Glu	Phe	Leu	Lys	Lys 520	Leu	Ser	Glu	Glu	Tyr 525	Gly	Lys	Lys
15	Leu	Glu 530	Glu	Leu	Ala	Glu	Lys 535	Ile	Tyr	Gln	Ile	Ala 540	Gly	Glu	Pro	Phe
	Asn 545	Ile	Asn	Ser	Pro	Lys 550	Gln	Val	Ser	Lys	Ile 555	Leu	Phe	Glu	Lys	Leu 560
20	Gly	Ile	Lys	Pro	Arg 565	Gly	Lys	Thr	Thr	Lys 570	Thr	Gly	Glu	Tyr	Ser 575	Thr
	Arg	Ile	Glu	Val 580	Leu	Glu	Glu	Ile	Ala 585		Glu	His	Glu	Ile 590	Val	Pro
	Leu	Ile	Leu 595	Glu	Tyr	Arg	Lys	Ile 600		Lys	Leu	Lys	Ser 605	Thr	Tyr	Ile
25	Asp	Thr 610		Pro	Lys	Leu	Val 615		Pro	Lys	Thr	Gly 620		Ile	His	Ala
	Ser 625		His	Gln	Thr	Gly 630		Ala	Thr	Gly	Arg 635		Ser	Ser	Ser	Asp 640
30	Pro	Asn	Leu	Gln	Asn 645		Pro	Thr	Lys	Ser 650		Glu	Gly	Lys	Glu 655	Ile
	Arg	Lys	Ala	Ile 660		Pro	Gln	Asp	Pro 665		Trp	Trp	lle	Val 670		Ala
	Asp	Туг	Ser 675		Ile	Glu	Leu	Arg 680		e Lev	. Ala	His	685		Gly	Asp
35	Glu	Asr 690		Val	Lys	Ala	Phe 695		ı Glu	ı Gly	, Ile	Asp 700		His	Thr	Leu

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val 730 725 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala 5 745 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser 760 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg 10 775 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp 790 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile 810 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp 15 820 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val 840 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu 20 850 855 860 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val 870 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 885 25 (2) INFORMATION FOR SEQ ID NO:8:

- - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 893 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: not relevant
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala

	Tyr	Tyr	Ala	Leu 20	Asp	Arg	Ser	Leu	Ser 25	Thr	Ser	Thr	Gly	Ile 30	Pro	Thr
	Asn	Ala	Val 35	Tyr	Gly	Val	Ala	Arg 40	Met	Leu	Val	Lys	Phe 45	Ile	Lys	Glu
5	His	Ile 50	Ile	Pro	Glu	Lys	Asp 55	Tyr	Ala	Ala	Val	Ala 60	Phe	Asp	Lys	Lys
	Ala 65	Ala	Thr	Phe	Arg	His 70	Lys	Leu	Leu	Val	Ser 75	Asp	Lys	Ala	Gln	Arg 80
10	Pro	Lys	Thr	Pro	Ala 85	Leu	Leu	Val	Gln	Gln 90	Leu	Pro	Tyr	Ile	Lys 95	Arg
	Leu	Ile	Glu	Ala 100	Leu	Gly	Phe	Lys	Val 105	Leu	Glu	Leu	Glu	Gly 110	Tyr	Glu
	Ala	Asp	Asp 115	Ile	Ile	Ala	Thr	Leu 120	Ala	Val	Arg	Ala	Ala 125	Arg	Phe	Leu
15	Met	Arg 130	Phe	Ser	Leu	Ile	Thr 135	Gly	Asp	Lys	Asp	Met 140	Leu	Gln	Leu	Val
	Asn 145	Glu	Lys	Ile	Lys	Val 150	Trp	Arg	Ile	Val	Lys 155	Gly	Ile	Ser	Asp	Leu 160
20	Glu	Leu	Tyr	Asp	Ser 165	Lys	Lys	Val	Lys	Glu 170	Arg	Tyr	Gly	Val	Glu 175	Pro
	His	Gln	Ile	Pro 180	Asp	Leu	Leu	Ala	Leu 185	Thr	Gly	Asp	Asp	Ile 190	Asp	Asn
	Ile	Pro	Asp 195	Val	Thr	Gly	Ile	Gly 200	Glu	Lys	Thr	Ala	Val 205	Gln	Leu	Leu
25	Gly	Lys 210	Tyr	Arg	Asn	Leu	Glu 215	Туг	Ile	Leu	Glu	His 220	Ala	Arg	Glu	Leu
	Pro 225	Gln	Arg	Val	Arg	Lys 230	Ala	Leu	Leu	Arg	Asp 235	Arg	Glu	Val	Ala	Ile 240
30	Leu	Ser	Lys	Lys	Leu 245	Ala	Thr	Leu	Val	Thr 250	Asn	Ala	Pro	Val	Glu 255	Val
	Asp	Trp	Glu	Glu 260	Met	Lys	Tyr	Arg	Gly 265	Tyr	Asp	Lys	Arg	Lys 270	Leu	Leu
	Pro	Ile	Leu 275	Lys	Glu	Leu	Glu	Phe 280	Ala	Ser	Ile	Met	Lys 285	Glu	Leu	Gln
35	Leu	Tyr 290	Glu	Glu	Ala	Glu	Pro 295	Thr	Gly	Tyr	Glu	Ile 300	Val	Lys	Asp	His

	Lys 305	Thr	Phe	Glu	Asp	Leu 310	Ile	Glu	Lys	Leu	Lys 315	Glu	Val	Pro	Ser	Phe 320
	Ala	Leu	Ala	Leu	Glu 325	Thr	Ser	Ser	Leu	Asp 330	Pro	Phe	Asn	Сув	Glu 335	Ile
5	Val	Gly	Ile	Ser 340	Val	Ser	Phe	Lys	Pro 345	Lys	Thr	Ala	Tyr	Tyr 350	Ile	Pro
	Leu	His	His 355	Arg	Asn	Ala	Gln	Asn 360	Leu	Asp	Glu	Thr	Leu 365	Val	Leu	Ser
10	Lys	Leu 370	Lys	Glu	Ile	Leu	Glu 375	Asp	Pro	Ser	Ser	Lys 380	Ile	Val	Gly	Gln
	Asn 385	Leu	Lys	Tyr	Asp	Tyr 390	Lys	Val	Leu	Met	Val 395	Lys	Gly	Ile	Ser	Pro 400
	Val	Tyr	Pro	His	Phe 405	Asp	Thr	Met	Ile	Ala 410	Ala	Tyr	Leu	Leu	Glu 415	Pro
15	Asn	Glu	Lys	Lys 420	Phe	Asn	Leu	Glu	Asp 425	Leu	Ser	Leu	Lys	Phe 430	Leu	Gly
	Туг	Lys	Met 435	Thr	Ser	Tyr	Gln	Glu 440	Leu	Met	Ser	Phe	Ser 445	Ser	Pro	Leu
20	Phe	Gly 450	Phe	Ser	Phe	Ala	Asp 455	Val	Pro	Val	Asp	Lys 460		Ala	Asn	Tyr
	Ser 465		Glu	Asp	Ala	Asp 470	Ile	Thr	Tyr	Arg	Leu 475	Tyr	Lys	Ile	Leu	Ser 480
	Met	Lys	Leu	His	Glu 485		Glu	Leu	Glu	Asn 490		Phe	Tyr	Arg	Ile 495	Glu
25	Met	Pro	Leu	Val 500		Val	Leu	Ala	Arg 505		Glu	Leu	Asn	Gly 510		Tyr
	Val	Asp	Thr 515		Phe	Leu	Lys	Lys 520		Ser	Glu	Glu	Tyr 525		Lys	Lys
30	Leu	Glu 530		Leu	Ala	Glu	Lys 535		туг	Gln	ılle	Ala 540		Glu	Pro	Phe
	Asr. 545		Asn	Ser	Pro	550		Val	Ser	Lys	555		ı Phe	Glu	Lys	Leu 560
	Gly	7 Ile	Lys	Pro	Arg 565		Lys	Thr	Thr	Буя 570		Gly	g Glu	Tyr	Ser 575	Thr
35	Arg	g Ile	e Glu	Val 580		ı Glu	ı Glu	ılle	Ala 585		ı Glu	ı His	s Glu	11e 590		Pro

	Leu	Ile	Leu 595	Glu	Tyr	Arg	Lys	Ile 600	Gln	Lys	Leu	Lys	Ser 605	Thr	Tyr	Ile
	Asp	Thr 610	Leu	Pro	Lys	Leu	Val 615	Asn	Pro	Lys	Thr	Gly 620	Arg	Ile	His	Ala
5	Ser 625	Phe	His	Gln	Thr	Gly 630	Thr	Ala	Thr	Gly	Arg 635	Leu	Ser	Ser	Ser	Asp 640
	Pro	Asn	Leu	Gln	Asn 645	Leu	Pro	Thr	Lys	Ser 650	Glu	Glu	Gly	Lys	Glu 655	Ile
10	Arg	Lys	Ala	Ile 660	Val	Pro	Gln	qaA	Pro 665	Asp	Trp	Trp	Ile	Val 670	Ser	Ala
	Asp	Tyr	Ser 675	Gln	Ile	Glu	Leu	Arg 680	Ile	Leu	Ala	His	Leu 685	Ser	Gly	Asp
	Glu	Asn 690	Leu	Val	Lys	Ala	Phe 695	Glu	Glu	Gly	Ile	Asp 700	Val	His	Thr	Leu
15	Thr 705	Ala	Ser	Arg	Ile	Tyr 710	Asn	Val	Lys	Pro	Glu 715	Glu	Val	Asn	Glu	Glu 720
	Met	Arg	Arg	Val	Gly 725	Lys	Met	Val	Asn	Phe 730	Ser	Ile	Ile	Tyr	Gly 735	Val
20	Thr	Pro	Туr	Gly 740	Leu	Ser	Val	Arg	Leu 745	Gly	Ile	Pro	Val	Lys 750	Glu	Ala
	Glu	Lys	Met 755	Ile	Ile	Ser	Tyr	Phe 760	Thr	Leu	Tyr	Pro	Lys 765	Val	Arg	Ser
	Tyr	11e 770		Gln	Val	Val	Ala 775	Glu	Ala	Lys	Glu	Lys 780		Tyr	Val	Arg
25	Thr 785		Phe	Gly	Arg	Lys 790	Arg	Asp	Ile	Pro	Gln 795		Met	Ala	Arg	Asp 800
	Lys	Asn	Thr	Gln	Ser 805		Gly	Glu	Arg	Ile 810		Ile	Asn	Thr	Pro 815	
30	Gln	Gly	Thr	Ala 820		. Asp	Ile	Ile	Lys 825		Ala	. Met	Ile	830		Asp
	Glu	Glu	Leu 835		Lys	Arg	Asn	Met 840		Ser	Arg	Met	11e 845		Gln	Val
	His	850		. Leu	val	Phe	61u 855		Pro	Asp	Glu	860		Glu	Glu	Leu
35	Val 865		Leu	ı Val	Lys	870		Met	Thr	Asn	Val 875		Lys	Leu	Ser	Val 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser 885 890

## (2) INFORMATION FOR SEQ ID NO:9:

141	CECTENCE	CHARACTERISTICS:	

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

### (ii) MOLECULE TYPE: protein

10	(vi)	SPOTTENCE	DESCRIPTION:	SEO	ID	NO:9:
10	(X1)	SECUENCE	DESCRIPTION.	250	11	110.5.

Met Ala Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala
1		5					10					15	

- Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr 20 25 30
- Asn Ala Val Tyr Asp Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
  35 40 45
  - His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys 50 55 60
- Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg

  70 75 80
  - Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
  - Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
    100 105 110
- 25 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu 115 120 125
  - Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val 130 135 140
- Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu 145 150 155 160
  - Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro 165 170 175
  - His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn 180 185 190
- 35 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu 195 200 205

	Gly Lya		Arg Asn	Leu	Glu 215	Tyr	Ile	Leu	Glu	His 220	Ala	Arg	Glu	Leu
	Pro Gla 225	n Arg V	Val Arg	Lys 230	Ala	Leu	Leu	Arg	Asp 235	Arg	Glu	Val	Ala	Ile 240
5	Leu Se	r Lys I	Lys Leu 245		Thr	Leu	Val	Thr 250	Asn	Ala	Pro	Val	Glu 255	Val
	Asp Tr	=	Glu Met 260	Lys	Tyr	Arg	Gly 265	Tyr	Asp	Lys	Arg	Lys 270	Leu	Leu
10	Pro Il	e Leu 1 275	Lys Glu	Leu	Glu	Phe 280	Ala	Ser	Ile	Met	Lys 285	Glu	Leu	Gln
	Leu Ty 29		Glu Ala	Glu	Pro 295	Thr	Gly	Tyr	Glu	Ile 300	Val	Lys	qaA	His
	Lys Th 305	r Phe (	Glu Asp	Leu 310	Ile	Glu	Lys	Leu	Lys 315	Glu	Val	Pro	Ser	Phe 320
15	Ala Le	u Ala :	Leu Glu 325		Ser	Ser	Leu	Asp 330	Pro	Phe	Asn	Cys	Glu 335	Ile
	Val Gl		Ser Val 340	. Ser	Phe	Lys	Pro 345	Lys	Thr	Ala	Tyr	Tyr 350	Ile	Pro
20	Leu Hi	s His 3	Arg Ası	n Ala	Gln	Asn 360	Leu	Asp	Glu	Thr	Leu 365	Val	Leu	Ser
	Lys Le		Glu Ile	e Leu	Glu 375	Asp	Pro	Ser	Ser	Lys 380	Ile	Val	Gly	Gln
	Asn Le 385	u Lys	Tyr Ası	390		Val	Leu	Met	Val 395	Lys	Gly	Ile	Ser	Pro 400
25	Val Ty	r Pro	His Pho		Thr	Met	Ile	Ala 410	Ala	Tyr	Leu	Leu	Glu 415	Pro
	Asn Gl		Lys Pho 420	e Asn	Leu	Glu	Asp 425		Ser	Leu	Lys	Phe 430	Leu	Gly
30	Tyr Ly	rs Met 435	Thr Se	r Tyr	Gln	Glu 440		Met	Ser	Phe	Ser 445		Pro	Leu
		ly Phe 50	Ser Ph	e Ala	Asp 455		Pro	Val	Asp	Lys 460		Ala	Asn	Tyr
	Ser Cy 465	ys Glu	Asp Al	a Asp 470		Thr	Tyr	Arg	Leu 475		Lys	Ile	Leu	Ser 480
35	Met Ly	ys Leu	His Gl 48		a Glu	Leu	Glu	490		Phe	туг	Arg	Ile 495	

	Met	Pro	Leu	Val 500	Asn	Val	Leu	Ala	Arg 505	Met	Glu	Leu	Asn	Gly 510	Val	Tyr
	Val	qaA	Thr 515	Glu	Phe	Leu	Lys	Lys 520	Leu	Ser	Glu	Glu	Tyr 525	Gly	Lys	Lys
5	Leu	Glu 530	Glu	Leu	Ala	Glu	Lys 535	Ile	Tyr	Gln	Ile	Ala 540	Gly	Glu	Pro	Phe
	Asn 545	Ile	Asn	Ser	Pro	Lys 550	Gln	Val	Ser	Lys	Ile 555	Leu	Phe	Glu	Lys	Leu 560
10	Gly	Ile	Lys	Pro	Arg 565	Gly	Lys	Thr	Thr	Lys 570	Thr	Gly	Glu	Tyr	Ser <b>5</b> 75	Thr
	Arg	Ile	Glu	Val 580	Leu	Glu	Glu	Ile	Ala 585	Asn	Glu	His	Glu	Ile 590	Val	Pro
	Leu	Ile	Leu 595	Glu	Tyr	Arg	Lys	Ile 600	Gln	Lys	Leu	Lys	Ser 605	Thr	Tyr	Ile
15	Asp	Thr 610	Leu	Pro	Lys	Leu	Val 615	Asn	Pro	Lys	Thr	Gly 620	Arg	Ile	His	Ala
	Ser 625	Phe	His	Gln	Thr	Gly 630	Thr	Ala	Thr	Gly	Arg 635	Leu	Ser	Ser	Ser	Asp 640
20	Pro	Asn	Leu	Gln	Asn 645	Leu	Pro	Thr	Lys	Ser 650	Glu	Glu	Gly	Lys	Glu 655	Ile
	Arg	Lys	Ala	Ile 660	Val	Pro	Gln	Asp	Pro 665	Asp	Trp	Trp	Ile	Val 670	Ser	Ala
	Asp	Tyr	Ser 675		Ile	Glu	Leu	Arg 680		Leu	Ala	His	Leu 685		Gly	Asp
25	Glu	Asn 690		Val	Lys	Ala	Phe 695		Glu	Gly	Ile	Asp 700		His	Thr	Leu
	Thr 705		. Ser	Arg	Ile	Tyr 710		Val	Lys	Pro	Glu 715		Val	Asn	Glu	Glu 720
30	Met	Arg	Arg	Val	Gly 725		Met	Val	Asn	730		Ile	lle	Tyr	Gly 735	Val
	Thr	Pro	туг	Gly 740		Ser	Val	Arg	745		Ile	Pro	Val	Lys 750		Ala
	Glu	і Гув	755		· Ile	s Ser	Tyr	760		Leu	Tyr	Pro	765		Arg	Ser
35	Туз	770		Glr.	val	. Val	. Ala		a Ala	Lys	: Glu	1 Lys 780		туг туг	Val	Arg

		Thr 785	Leu	Phe	Gly	Arg	Lys 790	Arg	qaA	Ile	Pro	Gln 795	Leu	Met	Ala	Arg	Asp 800
		Lys	Asn	Thr	Gln	Ser 805	Glu	Gly	Glu	Arg	Ile 810	Ala	Ile	Asn	Thr	Pro 815	Ile
5		Gln	Gly	Thr	Ala 820	Ala	Asp	Ile	Ile	Lys 825	Leu	Ala	Met	Ile	Asp 830	Ile	Asp
		Glu	Glu	Leu 835	Arg	Lys	Arg	Asn	Met 840	Lys	Ser	Arg	Met	Ile 845	Ile	Gln	Val
10		His	qaA 028	Glu	Leu	Val	Phe	Glu 855	Val	Pro	Asp	Glu	Glu 860	Lys	Glu	Glu	Leu
		Val 865	Ąsp	Leu	Val	Lys	Asn 870	Lys	Met	Thr	Asn	Val 875	Val	Lys	Leu	Ser	Val 880
		Pro	Leu	Glu	Val	Asp 885	Ile	Ser	Ile	Gly	Lys 890	Ser	Trp	Ser			
15	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID NO	0:10	:								
20		(i) (ii)	(A) (B) (C) (D)	JENCI ) LEI ) TYI ) STI ) TOI ECULI	NGTH PE: 8 RANDI POLO	: 610 amino EDNE: GY: 1	am: coac: ss: not:	ino a id not : rele	acid rele								
		(xi)	SEO	UENC:	E DE	SCRI	PTIO	n: S	EO I	D NO	:10:						
											Ala	Glu	Pro	Thr	Glv	Tvr	Glu
		1	пув	Giu	нец	5	neu	ıyı	OLU	Olu	10	014	110		017	15	0_0
25		Ile	Val	Lys	Asp 20	His	Lys	Thr	Phe	Glu 25	Asp	Leu	Ile	Glu	Lys 30	Leu	Lys
		Glu	Val	Pro 35	Ser	Phe	Ala	Leu	Asp 40	Leu	Glu	Thr	Ser	Ser 45	Leu	Asp	Pro
30		Phe	Asn 50	Сув	Glu	Ile	Val	Gly 55	Ile	Ser	Val	Ser	Phe 60	Lys	Pro	Lys	Thr
		Ala 65	Tyr	Tyr	Ile	Pro	Leu 70	His	His	Arg	Asn	Ala 75	Gln	Asn	Leu	Asp	Glu 80
		Thr	Leu	Val	Leu	Ser 85	Lys	Leu	Lys	Glu	Ile 90	Leu	Glu	Asp	Pro	Ser 95	Sei
35		Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Туг	Lys	Val	Leu	Met	Va]

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser 5 Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile 455 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr 10 Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu 490 Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala 15 520 Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg 20 550 Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu 570 565 Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val 585 580 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser 25 600 Trp Ser 610

(2) INFORMATION FOR SEQ ID NO:11:

- 30 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

	<ul><li>(A) NAME/KEY: Modified-site</li><li>(B) LOCATION: 114</li><li>(D) OTHER INFORMATION: /note= "'Xaa' is any amino acid</li></ul>
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
5	Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa 1 5 10
	(2) INFORMATION FOR SEQ ID NO:12:
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 14 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>
	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
15	Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly 1 5 10
	(2) INFORMATION FOR SEQ ID NO:13:
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 14 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>
	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
25	Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly 1 5 10
	(2) INFORMATION FOR SEQ ID NO:14:
30	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 14 amino acids</li><li>(B) TYPE: amino acid</li><li>(C) STRANDEDNESS: not relevant</li><li>(D) TOPOLOGY: linear</li></ul>

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
1 5 10

- (2) INFORMATION FOR SEQ ID NO:15:
- 5 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

- (2) INFORMATION FOR SEQ ID NO:16:
- 15 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly 1  $\phantom{0}$  5  $\phantom{0}$  10

- (2) INFORMATION FOR SEQ ID NO:17:
- 25 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly (2) INFORMATION FOR SEQ ID NO:18: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser 5 (2) INFORMATION FOR SEQ ID NO:19: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19: Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser (2) INFORMATION FOR SEQ ID NO:20: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:					
	Gly Pro Val Ala Phe Asp Ser Glu Thr Ser Ala 1 5 10					
	2) INFORMATION FOR SEQ ID NO:21:					
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>					
10	(ii) MOLECULE TYPE: peptide					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:					
	Met Ile Val Ser Asp Ile Glu Ala Asn Ala 1 5 10					
	(2) INFORMATION FOR SEQ ID NO:22:					
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>					
20	(ii) MOLECULE TYPE: cDNA					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:					
	GACGTTTCAA GCGCTAGGGC AAAAGA	26				
	(2) INFORMATION FOR SEQ ID NO:23:					
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 31 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>					
	(ii) MOLECULE TYPE: cDNA					
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:					

GTATATTATA GAGTAGTTAA CCATCTTTCC A

	(2)	INFORMATION FOR SEQ ID NO:24:
5		<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 6 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
10		Phe Leu Phe Asp Gly Thr 1 5
	(2)	INFORMATION FOR SEQ ID NO:25:
15		<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 6 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>
		(ii) MOLECULE TYPE: peptide
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
20		Leu Leu Val Asp Gly His 1 5
	(2)	INFORMATION FOR SEQ ID NO:26:
25		<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: not relevant</li> <li>(D) TOPOLOGY: linear</li> </ul>
		(ii) MOLECULE TYPE: peptide
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
30		Ser Leu Ile Thr Gly Asp Lys Asp Met Leu 1 5 10

(i) SEQUENCE CHARACTERISTICS:

5	(2)	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 10 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: not relevant  (D) TOPOLOGY: linear  MOLECULE TYPE: peptide	
10		Arg 1	SEQUENCE DESCRIPTION: SEQ ID NO:27:  Ile Leu Thr Ala Asp Lys Asp Leu Tyr 5 10	
15	(2)	(i)	RMATION FOR SEQ ID NO:28:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  MOLECULE TYPE: cDNA	
	GTA(		SEQUENCE DESCRIPTION: SEQ ID NO:28: GG GCTGTGCCGG CAAAGAGAAA TAGTC	35
<ul><li>20</li><li>25</li></ul>	(2)	(i)	RMATION FOR SEQ ID NO:29:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 35 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  MOLECULE TYPE: cDNA	
		GCATA	SEQUENCE DESCRIPTION: SEQ ID NO:29: TC CTTGGCGCCG GTTATTATGA AAATC RMATION FOR SEQ ID NO:30:	35

	<ul><li>(A) LENGTH: 30 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
	CACCAGACGG GTACCGCCAC TGGCAGGTTG	30
	(2) INFORMATION FOR SEQ ID NO:31:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 48 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
	TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTTCT TCGAACAC	48
	(2) INFORMATION FOR SEQ ID NO:32:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 48 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
25	TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTTCT TCGAACAC	48
	(2) INFORMATION FOR SEQ ID NO:33:	
30	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 48 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
	TATAGAGTAG TTAACCATCT TTCCAACCCG GTTCATTTCT TCGAACAC	48
	(2) INFORMATION FOR SEQ ID NO:34:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 48 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
10	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
	TATAGAGTAG TTAACCATCT TTCCAACCCG ATGCATTTCT TCGAACAC	48
	(2) INFORMATION FOR SEQ ID NO:35:	
15	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 29 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
	AAGATGGTTA ACGCGTCTAT AATATACGG	29
	(2) INFORMATION FOR SEQ ID NO:36:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	

		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
		CAAGAGGCAC AGAGAGTTTC ACC	23
		(2) INFORMATION FOR SEQ ID NO:37:	
	5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 30 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
	10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
		GTATATTATA GAGGAGTTAA CCATCTTTCC	30
		(2) INFORMATION FOR SEQ ID NO:38:	
	15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 29 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
E STATE OF THE STA		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
i pe	20	AAGATGGTTA ACTTCTCTAT AATATACGG	29
		(2) INFORMATION FOR SEQ ID NO:39:	
	25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 48 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

(2) INFORMATION FOR SEQ ID NO:40:

	5	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
		(ii)	MOLECULE TYPE: cDNA	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:40:	
		TATAGAGT	AG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC	48
	10	(2) INFO	RMATION FOR SEQ ID NO:41:	
	15	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
		(ii)	MOLECULE TYPE: cDNA	
\ \[		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:41:	
had had		CTTGGCCG	CC CGATGCATCA GGGGGTC	27
		(2) INFO	RMATION FOR SEQ ID NO:42:	
	20	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 30 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	25	(ii)	MOLECULE TYPE: cDNA	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
		CTTGGCCG	GCC CGCTTCATGA GGGGGTCCAC	30
		(2) INFO	ORMATION FOR SEQ ID NO:43:	
	30	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
	CTTGGCCGCC CTGTACATCA GGGGGTC	27
	(2) INFORMATION FOR SEQ ID NO:44:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 30 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
15	GTATATTATA GAGGTGTTAA CCATCTTTCC	30
	(2) INFORMATION FOR SEQ ID NO:45:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 34 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
	GGGAGACCGG AATTCTCCTT CATTAATTCC TATA	34
25	(2) INFORMATION FOR SEQ ID NO:46:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 49 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
30	(C) STRANDEDNESS: both (D) TOPOLOGY: both	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
	TGGAGACCCT GGAACTATAG GAATTAATGA AGGAGAATTC CGGTCTCCC	49
	(2) INFORMATION FOR SEQ ID NO:47:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
10	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
	GTATTTTGGT ATGCTTGTGC	20
	(2) INFORMATION FOR SEQ ID NO:48:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
	CTATTTTGGA ATATATGTGC CT	22
	(2) INFORMATION FOR SEQ ID NO:49:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	

TGCTCTCAGG ATTTCCTCCA

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
	ACGAACATTC TACAAGTTAC	20
	(2) INFORMATION FOR SEQ ID NO:50:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
10	(XI) SEQUENCE DESCRIPTION	20
	TTTCAGAGAA ACTGACCTGT	20
	(2) INFORMATION FOR SEQ ID NO:51:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
20	GATAAATGCC AAACATGTTG T	21
	(2) INFORMATION FOR SEQ ID NO:52:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	

		(2) INFORMATION FOR SEQ ID NO:53:	
	5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	20
		AGCTTGAGAC CTCTGTGTCC	20
	10	(2) INFORMATION FOR SEQ ID NO:54:	
	15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	22
=			
		(2) INFORMATION FOR SEQ ID NO:55:	
	20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	25	(ii) MOLECULE TYPE: cDNA	
		•	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
		TTGGAGTCGC AAGCTGAACT AGC	23
		(2) INFORMATION FOR SEQ ID NO:56:	
	30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
	GCCTGAGTGA CAGAGTGAGA ACC	23
	(2) INFORMATION FOR SEQ ID NO:57:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
15	CCCACTAGGT TGTAAGCTCC ATGA	24
	(2) INFORMATION FOR SEQ ID NO:58:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
	TACTATGTGC CAGGCTCTGT CCTA	24
25	(2) INFORMATION FOR SEQ ID NO:59:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
30	(C) STRANDEDNESS: both (D) TOPOLOGY: both	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	ACTCATGAAG GTGACAGTTC	20
	(2) INFORMATION FOR SEQ ID NO:60:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
10	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
	GTGTTGTTGA CCTATTGCAT	20
	(2) INFORMATION FOR SEQ ID NO:61:	
15	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
	ATCTCTGTTC CCTCCCTGTT	20
	(2) INFORMATION FOR SEQ ID NO:62:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	

TTTATGCGAG CGTATGGATA

(2) INFORMATION FOR SEQ ID NO:63:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (ii) MOLECULE TYPE: cDNA  (2) INFORMATION FOR SEQ ID NO:63:  (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:			
(2) INFORMATION FOR SEQ ID NO:63:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  AGCCCGTGTT GGAACCATGA CTG (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (II) MOLECULE TYPE: cDNA		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA  10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  AGCCCGTGTT GGAACCATGA CTG (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA		CTTATTGGCC TTGAAGGTAG	20
5 (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  AGCCCGTGTT GGAACCATGA CTG (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC (2) INFORMATION FOR SEQ ID NO:65: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA		(2) INFORMATION FOR SEQ ID NO:63:	
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  AGCCCGTGTT GGAACCATGA CTG  (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC  (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA	5	<ul><li>(A) LENGTH: 23 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li></ul>	
AGCCCGTGTT GGAACCATGA CTG  (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		(ii) MOLECULE TYPE: cDNA	
AGCCCGTGTT GGAACCATGA CTG  (2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA			
(2) INFORMATION FOR SEQ ID NO:64:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC 23 (2) INFORMATION FOR SEQ ID NO:65: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA	10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC  (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		AGCCCGTGTT GGAACCATGA CTG	23
(A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC 23 (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		(2) INFORMATION FOR SEQ ID NO:64:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  20 TACATAGCGA GACTCCATCT CCC  (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA	15	<ul><li>(A) LENGTH: 23 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li></ul>	
20 TACATAGCGA GACTCCATCT CCC  (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		(ii) MOLECULE TYPE: cDNA	
20 TACATAGCGA GACTCCATCT CCC  (2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA			
(2) INFORMATION FOR SEQ ID NO:65:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA	20	TACATAGCGA GACTCCATCT CCC	23
(A) LENGTH: 20 base pairs (B) TYPE: nucleic acid  (C) STRANDEDNESS: both (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA		(2) INFORMATION FOR SEQ ID NO:65:	
(ii) MOLECULE TYPE: cDNA	25	<ul><li>(A) LENGTH: 20 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
		(D) TOPOLOGY: both	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	

		(2) INFORMATION FOR SEQ ID NO:66:	
	5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
		CACCACCATT GATCTGGAAG	20
Print Print	10	(2) INFORMATION FOR SEQ ID NO:67:	
Norm Herr Norm 18" South Shrift Shrift	15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 16 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
-		(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	16
		CCAACCACAC TGGGAA	10
	20	(2) INFORMATION FOR SEQ ID NO:68:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 16 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	25	(ii) MOLECULE TYPE: cDNA	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
		AACAGTTGCC CACGGT	16
		(2) INFORMATION FOR SEQ ID NO:69:	
	30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
3	CATGAAATGC TGACTGGGTA	20
	(2) INFORMATION FOR SEQ ID NO:70:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
15	TCAATTTATG TGCAGCCAAT	20
	(2) INFORMATION FOR SEQ ID NO:71:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
	CATAGCGAGA CTCCATCTCC	20
25	(2) INFORMATION FOR SEQ ID NO:72:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	
30	(B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
	GGGAGAGGGC AAAGATCGAT	20
	(2) INFORMATION FOR SEQ ID NO:73:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
10	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
		22
	AACACTAGTG ACATTATTTT CA	
	(2) INFORMATION FOR SEQ ID NO:74:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
	AGCTAGGCCT GAAGGCTTCT	20
	(2) INFORMATION FOR SEQ ID NO:75:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	

ATTTGGATGG CTTGACAGAG

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
	CCCTAGTGGA TGATAAGAAT AATC	24
	(2) INFORMATION FOR SEQ ID NO:76:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 30 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
	GGACAGATGA TAAATACATA GGATGGATGG	30
	(2) INFORMATION FOR SEQ ID NO:77:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
20	TTCTCTTACA ACACTGCCCC	20
	(2) INFORMATION FOR SEQ ID NO:78:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	

	(2) INFORMATION FOR SEQ ID NO:79:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
	ACATTCTAAG ACTTTCCCAA T	21
10	(2) INFORMATION FOR SEQ ID NO:80:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
	AGAGCATGCA CCCTGAATTG	20
	(2) INFORMATION FOR SEQ ID NO:81:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
25	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
	AAGAACCATG CGATACGACT	20
	(2) INFORMATION FOR SEQ ID NO:82:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
	CATTCCTAGA TGGGTAAAGC	20
	(2) INFORMATION FOR SEQ ID NO:83:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
15	GCTTAGTCAT ACGAGCGG	18
	(2) INFORMATION FOR SEQ ID NO:84:	
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 18 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
	TCCACAGCCA TGTAAACC	18
25	(2) INFORMATION FOR SEQ ID NO:85:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 16 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
30	(C) STRANDEDNESS: both (D) TOPOLOGY: both	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
	CCCCGGAGCA AGTTCA	16
	(2) INFORMATION FOR SEQ ID NO:86:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
10	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
	CAGCCCAAAG CCAGATTA	18
	(2) INFORMATION FOR SEQ ID NO:87:	
15	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: both</li><li>(D) TOPOLOGY: both</li></ul>	
	(ii) MOLECULE TYPE: cDNA	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
	ATATGTGAGT CAATTCCCCA AG	22
	(2) INFORMATION FOR SEQ ID NO:88:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both	
	(ii) MOLECULE TYPE: cDNA	

ATTCTGGGCG CACAAGAGTG A

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
	TGTATTAGTC AATGTTCTCC AG	22
	(2) INFORMATION FOR SEQ ID NO:89:	
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 19 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
	CAGCTGCCCT AGTCAGCAC	19
	(2) INFORMATION FOR SEQ ID NO:90:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
20	GCTTCCGAGT GCAGGTCACA	20
	(2) INFORMATION FOR SEQ ID NO:91:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(*;) SECTIENCE DESCRIPTION: SEC ID NO.91:	

(2) INFORMATION FOR SEQ ID NO:92:

	5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: both  (D) TOPOLOGY: both  (ii) MOLECULE TYPE: cDNA	
٠		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
		ACATCTCCCC TACCGCTATA	20
C_	10	(2) INFORMATION FOR SEQ ID NO:93:	
	15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: both</li> <li>(D) TOPOLOGY: both</li> </ul>	
		(ii) MOLECULE TYPE: cDNA	
y		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
		GAAGTTCACC ATCCGGCCGA CCCGTCGCAT TTC	33